

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: RUEGER, DAVID C.  
KUBERASAMPATH, THANGAVEL  
OPPERMANN, HERMANN  
OZKAYNAK ENGIN  
PANG, ROY H.L.  
COHEN, CHARLES M.
- (ii) TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND REPAIR
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
(B) STREET: 53 STATE STREET  
(C) CITY: BOSTON  
(D) STATE: MASSACHUSETTS  
(E) COUNTRY: U.S.A.  
(F) ZIP: 02109
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 667,274  
(B) FILING DATE: 11-MAR-1991
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 752,764  
(B) FILING DATE:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 97 amino acids  
(B) TYPE: amino acids  
(C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:  
(A) NAME: Generic Sequence 1

0037756-09297  
265260-9524680

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer,  $\alpha$ -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Xaa Xaa Xaa Xaa Xaa Xaa
 1                               5
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 10                             15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 20                             25
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 30                             35
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 40                             45                             50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 55                             60
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65                             70
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 75                             80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 85                             90
Xaa Cys Xaa
 95

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 2

08937756-092597

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer,  $\alpha$ -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Xaa Xaa Xaa Xaa Xaa Xaa
  1                               5
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 10                               15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 20                               25
Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 30                               35
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 40                               45                               50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 55                               60
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65                               70
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 75                               80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 85                               90
Xaa Cys Xaa
 95

```

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acids
  - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

08937756.082597

—

(D) OTHER INFORMATION: wherein each

— — —

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Tyr Val Xaa Phe

1 5

Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

10

Xaa Ala Pro Gly Xaa Xaa Xaa Ala

15 20

Xaa Tyr Cys Xaa Gly Xaa Cys Xaa

25 30

Xaa Pro Xaa Xaa Xaa Xaa Xaa

35

Xaa Xaa Xaa Asn His Ala Xaa Xaa

40 45

Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa

50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

55 60

Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

65

Xaa Xaa Xaa Leu Xaa Xaa Xaa

70 75

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

80

Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85 90

**BIBLIOGRAPHY**



Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
60 65  
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa  
70  
Xaa Xaa Xaa Leu Xaa Xaa Xaa  
75 80  
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa  
85  
Xaa Xaa Xaa Xaa Met Xaa Val Xaa  
90 95  
Xaa Cys Gly Cys Xaa  
100

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 139 amino acids
    - (B) TYPE: amino acids
    - (C) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (A) NAME: hOP-1 (mature form)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Gly | Ser | Lys | Gln | Arg | Ser | Gln |
| 1   |     |     |     | 5   |     |     |     |     |
| Asn | Arg | Ser | Lys | Thr | Pro | Lys | Asn | Gln |
| 10  |     |     |     |     | 15  |     |     |     |
| Glu | Ala | Leu | Arg | Met | Ala | Asn | Val | Ala |
|     | 20  |     |     |     |     | 25  |     |     |
| Glu | Asn | Ser | Ser | Ser | Asp | Gln | Arg | Gln |
|     |     | 30  |     |     |     |     | 35  |     |
| Ala | Cys | Lys | Lys | His | Glu | Leu | Tyr | Val |
|     |     |     | 40  |     |     |     |     | 45  |
| Ser | Phe | Arg | Asp | Leu | Gly | Trp | Gln | Asp |
|     |     |     |     | 50  |     |     |     |     |

20250909 09:56:00

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Ile | Ala | Pro | Glu | Gly | Tyr | Ala |
| 55  |     |     |     |     | 60  |     |     |     |
| Ala | Tyr | Tyr | Cys | Glu | Gly | Glu | Cys | Ala |
|     | 65  |     |     |     |     | 70  |     |     |
| Phe | Pro | Leu | Asn | Ser | Tyr | Met | Asn | Ala |
|     |     | 75  |     |     |     |     | 80  |     |
| Thr | Asn | His | Ala | Ile | Val | Gln | Thr | Leu |
|     |     |     | 85  |     |     |     |     | 90  |
| Val | His | Phe | Ile | Asn | Pro | Glu | Thr | Val |
|     |     |     |     | 95  |     |     |     |     |
| Pro | Lys | Pro | Cys | Cys | Ala | Pro | Thr | Gln |
| 100 |     |     |     |     | 105 |     |     |     |
| Leu | Asn | Ala | Ile | Ser | Val | Leu | Tyr | Phe |
|     | 110 |     |     |     |     | 115 |     |     |
| Asp | Asp | Ser | Ser | Asn | Val | Ile | Leu | Lys |
|     |     | 120 |     |     |     |     | 125 |     |
| Lys | Tyr | Arg | Asn | Met | Val | Val | Arg | Ala |
|     |     |     | 130 |     |     |     |     | 135 |
| Cys | Gly | Cys | His |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 139 amino acids
    - (B) TYPE: amino acids
    - (C) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (A) NAME: mOP-1 (mature form)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Gly | Gly | Lys | Gln | Arg | Ser | Gln |
| 1   |     |     |     | 5   |     |     |     |     |

0893756-092597

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Arg | Ser | Lys | Thr | Pro | Lys | Asn | Gln |
| 10  |     |     |     |     | 15  |     |     |     |
| Glu | Ala | Leu | Arg | Met | Ala | Ser | Val | Ala |
|     | 20  |     |     |     |     | 25  |     |     |
| Glu | Asn | Ser | Ser | Ser | Asp | Gln | Arg | Gln |
|     |     | 30  |     |     |     |     | 35  |     |
| Ala | Cys | Lys | Lys | His | Glu | Leu | Tyr | Val |
|     |     |     | 40  |     |     |     |     | 45  |
| Ser | Phe | Arg | Asp | Leu | Gly | Trp | Gln | Asp |
|     |     |     | 50  |     |     |     |     |     |
| Trp | Ile | Ile | Ala | Pro | Glu | Gly | Tyr | Ala |
| 55  |     |     |     |     | 60  |     |     |     |
| Ala | Tyr | Tyr | Cys | Glu | Gly | Glu | Cys | Ala |
|     | 65  |     |     |     |     | 70  |     |     |
| Phe | Pro | Leu | Asn | Ser | Tyr | Met | Asn | Ala |
|     |     | 75  |     |     |     |     | 80  |     |
| Thr | Asn | His | Ala | Ile | Val | Gln | Thr | Leu |
|     |     |     | 85  |     |     |     |     | 90  |
| Val | His | Phe | Ile | Asn | Pro | Asp | Thr | Val |
|     |     |     | 95  |     |     |     |     |     |
| Pro | Lys | Pro | Cys | Cys | Ala | Pro | Thr | Gln |
| 100 |     |     |     |     | 105 |     |     |     |
| Leu | Asn | Ala | Ile | Ser | Val | Leu | Tyr | Phe |
|     | 110 |     |     |     |     | 115 |     |     |
| Asp | Asp | Ser | Ser | Asn | Val | Ile | Leu | Lys |
|     |     | 120 |     |     |     |     | 125 |     |
| Lys | Tyr | Arg | Asn | Met | Val | Val | Arg | Ala |
|     |     |     | 130 |     |     |     |     | 135 |
| Cys | Gly | Cys | His |     |     |     |     |     |

(2)

INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

0093756-093697



(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: hOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Arg | Pro | Leu | Arg | Arg | Arg | Gln |
| 1   |     |     |     | 5   |     |     |     |     |
| Pro | Lys | Lys | Ser | Asn | Glu | Leu | Pro | Gln |
| 10  |     |     |     |     | 15  |     |     |     |
| Ala | Asn | Arg | Leu | Pro | Gly | Ile | Phe | Asp |
| 20  |     |     |     |     |     | 25  |     |     |
| Asp | Val | His | Gly | Ser | His | Gly | Arg | Gln |
|     |     | 30  |     |     |     |     | 35  |     |
| Val | Cys | Arg | Arg | His | Glu | Leu | Tyr | Val |
|     |     |     | 40  |     |     |     |     | 45  |
| Ser | Phe | Gln | Asp | Leu | Gly | Trp | Leu | Asp |
|     |     |     |     | 50  |     |     |     |     |
| Trp | Val | Ile | Ala | Pro | Gln | Gly | Tyr | Ser |
| 55  |     |     |     |     | 60  |     |     |     |
| Ala | Tyr | Tyr | Cys | Glu | Gly | Glu | Cys | Ser |
| 65  |     |     |     |     |     | 70  |     |     |
| Phe | Pro | Leu | Asp | Ser | Cys | Met | Asn | Ala |
|     |     | 75  |     |     |     |     | 80  |     |
| Thr | Asn | His | Ala | Ile | Leu | Gln | Ser | Leu |
|     |     |     | 85  |     |     |     |     | 90  |
| Val | His | Leu | Met | Lys | Pro | Asn | Ala | Val |
|     |     |     |     | 95  |     |     |     |     |
| Pro | Lys | Ala | Cys | Cys | Ala | Pro | Thr | Lys |
| 100 |     |     |     |     | 105 |     |     |     |
| Leu | Ser | Ala | Thr | Ser | Val | Leu | Tyr | Tyr |
| 110 |     |     |     |     |     | 115 |     |     |
| Asp | Ser | Ser | Asn | Asn | Val | Ile | Leu | Arg |
|     |     | 120 |     |     |     |     | 125 |     |
| Lys | His | Arg | Asn | Met | Val | Val | Lys | Ala |
|     |     |     | 130 |     |     |     |     | 135 |
| Cys | Gly | Cys | His |     |     |     |     |     |

0033756-0924

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: mOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Arg | Pro | Leu | Lys | Arg | Arg | Gln |
| 1   |     |     |     | 5   |     |     |     |     |
| Pro | Lys | Lys | Thr | Asn | Glu | Leu | Pro | His |
| 10  |     |     |     |     | 15  |     |     |     |
| Pro | Asn | Lys | Leu | Pro | Gly | Ile | Phe | Asp |
|     | 20  |     |     |     |     | 25  |     |     |
| Asp | Gly | His | Gly | Ser | Arg | Gly | Arg | Glu |
|     |     | 30  |     |     |     |     | 35  |     |
| Val | Cys | Arg | Arg | His | Glu | Leu | Tyr | Val |
|     |     |     | 40  |     |     |     |     | 45  |
| Ser | Phe | Arg | Asp | Leu | Gly | Trp | Leu | Asp |
|     |     |     |     | 50  |     |     |     |     |
| Trp | Val | Ile | Ala | Pro | Gln | Gly | Tyr | Ser |
|     |     |     |     |     | 60  |     |     |     |
| Ala | Tyr | Tyr | Cys | Glu | Gly | Glu | Cys | Ala |
|     | 65  |     |     |     |     | 70  |     |     |
| Phe | Pro | Leu | Asp | Ser | Cys | Met | Asn | Ala |
|     |     | 75  |     |     |     |     | 80  |     |
| Thr | Asn | His | Ala | Ile | Leu | Gln | Ser | Leu |
|     |     |     | 85  |     |     |     |     | 90  |
| Val | His | Leu | Met | Lys | Pro | Asp | Val | Val |
|     |     |     |     | 95  |     |     |     |     |
| Pro | Lys | Ala | Cys | Cys | Ala | Pro | Thr | Lys |
| 100 |     |     |     |     | 105 |     |     |     |

00937756-09597

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ala | Thr | Ser | Val | Leu | Tyr | Tyr |
|     | 110 |     |     |     |     | 115 |     |     |
| Asp | Ser | Ser | Asn | Asn | Val | Ile | Leu | Arg |
|     |     | 120 |     |     |     |     | 125 |     |
| Lys | His | Arg | Asn | Met | Val | Val | Lys | Ala |
|     |     |     | 130 |     |     |     |     | 135 |
| Cys | Gly | Cys | His |     |     |     |     |     |

(2)

INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: CBMP-2A(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Lys | Arg | His | Pro | Leu | Tyr | Val | Asp | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |
| Asp | Val | Gly | Trp | Asn | Asp | Trp | Ile | Val | Ala | Pro |
|     |     | 15  |     |     |     |     |     | 20  |     |     |
| Pro | Gly | Tyr | His | Ala | Phe | Tyr | Cys | His | Gly | Glu |
|     |     | 25  |     |     |     |     | 30  |     |     |     |
| Cys | Pro | Phe | Pro | Leu | Ala | Asp | His | Leu | Asn | Ser |
|     | 35  |     |     |     |     | 40  |     |     |     |     |
| Thr | Asn | His | Ala | Ile | Val | Gln | Thr | Leu | Val | Asn |
| 45  |     |     |     | 50  |     |     |     |     | 55  |     |
| Ser | Val | Asn | Ser | Lys | Ile | Pro | Lys | Ala | Cys | Cys |
|     |     | 60  |     |     |     |     |     |     | 65  |     |

00037756.092597

Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu  
70 75  
Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys  
80 85  
Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly  
90 95  
Cys Arg  
100

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME: CBMP-2B(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Arg Arg His Ser  
1 5  
Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn  
10 15  
Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala  
20 25  
Phe Tyr Cys His Gly Asp Cys Pro Phe Pro Leu  
30 35  
Ala Asp His Leu Asn Ser Thr Asn His Ala Ile  
40 45  
Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser  
50 55 60  
Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu  
65 70

0093756-092597  
465260-9542680

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Ile | Ser | Met | Leu | Tyr | Leu | Asp | Glu | Tyr |
|     |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Lys | Val | Val | Leu | Lys | Asn | Tyr | Gln | Glu | Met |
|     |     |     |     |     | 85  |     |     |     | 90  |     |
| Val | Val | Glu | Gly | Cys | Gly | Cys | Arg |     |     |     |
|     |     |     |     |     | 95  |     |     |     | 100 |     |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: DPP(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Arg | Arg | His | Ser | Leu | Tyr | Val | Asp | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |
| Asp | Val | Gly | Trp | Asp | Asp | Trp | Ile | Val | Ala | Pro |
|     |     |     |     | 15  |     |     |     |     | 20  |     |
| Leu | Gly | Tyr | Asp | Ala | Tyr | Tyr | Cys | His | Gly | Lys |
|     |     |     |     | 25  |     |     |     |     | 30  |     |
| Cys | Pro | Phe | Pro | Leu | Ala | Asp | His | Phe | Asn | Ser |
|     |     |     |     | 35  |     |     |     |     | 40  |     |
| Thr | Asn | His | Ala | Val | Val | Gln | Thr | Leu | Val | Asn |
|     |     |     |     | 45  |     |     |     |     | 50  |     |
| Asn | Asn | Asn | Pro | Gly | Lys | Val | Pro | Lys | Ala | Cys |
|     |     |     |     | 60  |     |     |     |     | 65  |     |
| Cys | Val | Pro | Thr | Gln | Leu | Asp | Ser | Val | Ala | Met |
|     |     |     |     | 70  |     |     |     |     | 75  |     |

0893756.09597  
165260"9522680

Leu Tyr Leu Asn Asp Gln Ser Thr Val Val Leu  
 80 85  
 Lys Asn Tyr Gln Glu Met Thr Val Val Gly Cys  
 90 95  
 Gly Cys Arg  
 100

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Vgl(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys  
 1 5 10  
 Asp Val Gly Trp Gln Asn Trp Val Ile Ala Pro  
 15 20  
 Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly Glu  
 25 30  
 Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly  
 35 40  
 Ser Asn His Ala Ile Leu Gln Thr Leu Val His  
 45 50 55  
 Ser Ile Glu Pro Glu Asp Ile Pro Leu Pro Cys  
 60 65  
 Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met  
 70 75

003756-00597  
 465360-9542630

Leu Phe Tyr Asp Asn Asn Asp Asn Val Val Leu  
80 85  
Arg His Tyr Glu Asn Met Ala Val Asp Glu Cys  
90 95  
Gly Cys Arg  
100

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Vgr-1(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln  
1 5 10  
Asp Val Gly Trp Gln Asp Trp Ile Ile Ala Pro  
15 20  
Xaa Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu  
25 30  
Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala  
35 40  
Thr Asn His Ala Ile Val Gln Thr Leu Val His  
45 50 55  
Val Met Asn Pro Glu Tyr Val Pro Lys Pro Cys  
60 65  
Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val  
70 75

265260" 95426530

Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu  
80 85  
Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys  
90 95  
Gly Cys His  
100

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: human
- (F) TISSUE TYPE: BRAIN

- (ix) FEATURE:
- (D) OTHER INFORMATION:  
/product= "GDF-1 (fx)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly  
1 5 10  
Trp His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr  
15 20 25  
Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly  
30 35 40  
Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His  
45 50 55  
Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala  
60 65 70  
Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn  
75 80 85  
Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly  
90 95 100  
Cys Arg  
105

08937756-092597  
165260-952680



(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1822 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS
- (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 49..1341
- (D) OTHER INFORMATION: /standard\_name= "hOP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|  |     |
|--|-----|
| GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG | 57  |
| Met His Val  |     |
| 1  |     |
| CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA  | 105 |
| Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala  |     |
| 5 10 15  |     |
| CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC  | 153 |
| Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn  |     |
| 20 25 30 35  |     |
| GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG  | 201 |
| Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg  |     |
| 40 45 50   |     |

0093755-0959

|   |     |
|---|-----|
| CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC<br>Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg<br>55 60 65        | 249 |
| CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG<br>Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met<br>70 75 80        | 297 |
| CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC<br>Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly<br>85 90 95        | 345 |
| GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC<br>Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly<br>100 105 110 115 | 393 |
| CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC<br>Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp<br>120 125 130     | 441 |
| ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC<br>Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe<br>135 140 145     | 489 |
| CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC<br>His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile<br>150 155 160     | 537 |
| CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC<br>Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp<br>165 170 175     | 585 |
| TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT<br>Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr<br>180 185 190 195 | 633 |
| CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC<br>Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu<br>200 205 210     | 681 |
| GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC<br>Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp<br>215 220 225     | 729 |
| ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG<br>Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu<br>230 235 240     | 777 |
| GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC<br>Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro<br>245 250 255     | 825 |

00937" 9572680

|   |      |
|---|------|
| AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC<br>Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro<br>260 265 270 275 | 873  |
| TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC<br>Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile<br>280 285 290     | 921  |
| CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC<br>Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro<br>295 300 305     | 969  |
| AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC<br>Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser<br>310 315 320     | 1017 |
| AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC<br>Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe<br>325 330 335     | 1065 |
| CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC<br>Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala<br>340 345 350 355 | 1113 |
| GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG<br>Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met<br>360 365 370     | 1161 |
| AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC<br>Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn<br>375 380 385     | 1209 |
| CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC<br>Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala<br>390 395 400     | 1257 |
| ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA<br>Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys<br>405 410 415     | 1305 |
| TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC<br>Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His<br>420 425 430                          | 1351 |
| GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGCCAG  | 1411 |
| GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG   | 1471 |
| TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC   | 1531 |
| ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC   | 1591 |

0093756 "092597"

GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651  
CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711  
GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771  
CTGTAATAAA TGTACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /Product="OP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Val | Arg | Ser | Leu | Arg | Ala | Ala | Ala | Pro | His | Ser | Phe | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Trp | Ala | Pro | Leu | Phe | Leu | Leu | Arg | Ser | Ala | Leu | Ala | Asp | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asp | Asn | Glu | Val | His | Ser | Ser | Phe | Ile | His | Arg | Arg | Leu | Arg | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Glu | Arg | Arg | Glu | Met | Gln | Arg | Glu | Ile | Leu | Ser | Ile | Leu | Gly | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Pro | His | Arg | Pro | Arg | Pro | His | Leu | Gln | Gly | Lys | His | Asn | Ser | Ala | Pro |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     |     | 80  |
| Met | Phe | Met | Leu | Asp | Leu | Tyr | Asn | Ala | Met | Ala | Val | Glu | Glu | Gly | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Pro | Gly | Gly | Gln | Gly | Phe | Ser | Tyr | Pro | Tyr | Lys | Ala | Val | Phe | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Gln | Gly | Pro | Pro | Leu | Ala | Ser | Leu | Gln | Asp | Ser | His | Phe | Leu | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ala | Asp | Met | Val | Met | Ser | Phe | Val | Asn | Leu | Val | Glu | His | Asp | Lys |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Glu | Phe | Phe | His | Pro | Arg | Tyr | His | His | Arg | Glu | Phe | Arg | Phe | Asp | Leu |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

08937756-09697

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ile | Pro | Glu | Gly | Glu | Ala | Val | Thr | Ala | Ala | Glu | Phe | Arg | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Lys | Asp | Tyr | Ile | Arg | Glu | Arg | Phe | Asp | Asn | Glu | Thr | Phe | Arg | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Val | Tyr | Gln | Val | Leu | Gln | Glu | His | Leu | Gly | Arg | Glu | Ser | Asp | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Leu | Leu | Asp | Ser | Arg | Thr | Leu | Trp | Ala | Ser | Glu | Glu | Gly | Trp | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Phe | Asp | Ile | Thr | Ala | Thr | Ser | Asn | His | Trp | Val | Val | Asn | Pro | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Asn | Leu | Gly | Leu | Gln | Leu | Ser | Val | Glu | Thr | Leu | Asp | Gly | Gln | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Asn | Pro | Lys | Leu | Ala | Gly | Leu | Ile | Gly | Arg | His | Gly | Pro | Gln | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Gln | Pro | Phe | Met | Val | Ala | Phe | Phe | Lys | Ala | Thr | Glu | Val | His | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Ser | Ile | Arg | Ser | Thr | Gly | Ser | Lys | Gln | Arg | Ser | Gln | Asn | Arg | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Thr | Pro | Lys | Asn | Gln | Glu | Ala | Leu | Arg | Met | Ala | Asn | Val | Ala | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Ser | Ser | Ser | Asp | Gln | Arg | Gln | Ala | Cys | Lys | Lys | His | Glu | Leu | Tyr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Ser | Phe | Arg | Asp | Leu | Gly | Trp | Gln | Asp | Trp | Ile | Ile | Ala | Pro | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Tyr | Ala | Ala | Tyr | Tyr | Cys | Glu | Gly | Glu | Cys | Ala | Phe | Pro | Leu | Asn |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Tyr | Met | Asn | Ala | Thr | Asn | His | Ala | Ile | Val | Gln | Thr | Leu | Val | His |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Phe | Ile | Asn | Pro | Glu | Thr | Val | Pro | Lys | Pro | Cys | Cys | Ala | Pro | Thr | Gln |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Asn | Ala | Ile | Ser | Val | Leu | Tyr | Phe | Asp | Asp | Ser | Ser | Asn | Val | Ile |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Lys | Lys | Tyr | Arg | Asn | Met | Val | Val | Arg | Ala | Cys | Gly | Cys | His |     |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1873 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: MURIDAE
  - (F) TISSUE TYPE: EMBRYO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 104..1393
  - (D) OTHER INFORMATION: /note= "MOP1 (CDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|   |                 |
|---|-----------------|
| CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCCTCCGCTG CCACCTGGGG | 60              |
| CGGCGCGGGC CCGGTGCCCC GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC   | 115             |
|   | Met His Val Arg |
|   | 1               |
| TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT   | 163             |
| Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro   |                 |
| 5 10 15 20  |                 |
| CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG   | 211             |
| Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu   |                 |
| 25 30 35  |                 |
| GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG   | 259             |
| Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg   |                 |
| 40 45 50  |                 |
| GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CCG   | 307             |
| Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro   |                 |
| 55 60 65  |                 |
| CGC CCG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG   | 355             |
| Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu   |                 |
| 70 75 80  |                 |
| GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG AGC GGG CCG GAC GGA CAG   | 403             |
| Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln   |                 |
| 85 90 95 100  |                 |

265260" 9544680

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GGC | TTC | TCC | TAC | CCC | TAC | AAG | GCC | GTC | TTC | AGT | ACC | CAG | GGC | CCC | CCT | 451  |
| Gly | Phe | Ser | Tyr | Pro | Tyr | Lys | Ala | Val | Phe | Ser | Thr | Gln | Gly | Pro | Pro |      |
|     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |      |
| TTA | GCC | AGC | CTG | CAG | GAC | AGC | CAT | TTC | CTC | ACT | GAC | GCC | GAC | ATG | GTC | 499  |
| Leu | Ala | Ser | Leu | Gln | Asp | Ser | His | Phe | Leu | Thr | Asp | Ala | Asp | Met | Val |      |
|     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |     |      |
| ATG | AGC | TTC | GTC | AAC | CTA | GTG | GAA | CAT | GAC | AAA | GAA | TTC | TTC | CAC | CCT | 547  |
| Met | Ser | Phe | Val | Asn | Leu | Val | Glu | His | Asp | Lys | Glu | Phe | Phe | His | Pro |      |
|     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |      |
| CGA | TAC | CAC | CAT | CGG | GAG | TTC | CGG | TTT | GAT | CTT | TCC | AAG | ATC | CCC | GAG | 595  |
| Arg | Tyr | His | His | Arg | Glu | Phe | Arg | Phe | Asp | Leu | Ser | Lys | Ile | Pro | Glu |      |
|     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     |      |
| GGC | GAA | CGG | GTG | ACC | GCA | GCC | GAA | TTC | AGG | ATC | TAT | AAG | GAC | TAC | ATC | 643  |
| Gly | Glu | Arg | Val | Thr | Ala | Ala | Glu | Phe | Arg | Ile | Tyr | Lys | Asp | Tyr | Ile |      |
|     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |      |
| CGG | GAG | CGA | TTT | GAC | AAC | GAG | ACC | TTC | CAG | ATC | ACA | GTC | TAT | CAG | GTG | 691  |
| Arg | Glu | Arg | Phe | Asp | Asn | Glu | Thr | Phe | Gln | Ile | Thr | Val | Tyr | Gln | Val |      |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |      |
| CTC | CAG | GAG | CAC | TCA | GGC | AGG | GAG | TCG | GAC | CTC | TTC | TTG | CTG | GAC | AGC | 739  |
| Leu | Gln | Glu | His | Ser | Gly | Arg | Glu | Ser | Asp | Leu | Phe | Leu | Leu | Asp | Ser |      |
|     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |     |      |
| CGC | ACC | ATC | TGG | GCT | TCT | GAG | GAG | GGC | TGG | TTG | GTG | TTT | GAT | ATC | ACA | 787  |
| Arg | Thr | Ile | Trp | Ala | Ser | Glu | Glu | Gly | Trp | Leu | Val | Phe | Asp | Ile | Thr |      |
|     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |      |
| GCC | ACC | AGC | AAC | CAC | TGG | GTG | GTC | AAC | CCT | CGG | CAC | AAC | CTG | GGC | TTA | 835  |
| Ala | Thr | Ser | Asn | His | Trp | Val | Val | Asn | Pro | Arg | His | Asn | Leu | Gly | Leu |      |
|     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |     |     |     |      |
| CAG | CTC | TCT | GTG | GAG | ACC | CTG | GAT | GGG | CAG | AGC | ATC | AAC | CCC | AAG | TTG | 883  |
| Gln | Leu | Ser | Val | Glu | Thr | Leu | Asp | Gly | Gln | Ser | Ile | Asn | Pro | Lys | Leu |      |
|     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     | 260 |      |
| GCA | GGC | CTG | ATT | GGA | CGG | CAT | GGA | CCC | CAG | AAC | AAG | CAA | CCC | TTC | ATG | 931  |
| Ala | Gly | Leu | Ile | Gly | Arg | His | Gly | Pro | Gln | Asn | Lys | Gln | Pro | Phe | Met |      |
|     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |     | 275 |     |      |
| GTG | GCC | TTC | TTC | AAG | GCC | ACG | GAA | GTC | CAT | CTC | CGT | AGT | ATC | CGG | TCC | 979  |
| Val | Ala | Phe | Phe | Lys | Ala | Thr | Glu | Val | His | Leu | Arg | Ser | Ile | Arg | Ser |      |
|     |     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |     |     |      |
| ACG | GGG | GGC | AAG | CAG | CGC | AGC | CAG | AAT | CGC | TCC | AAG | ACG | CCA | AAG | AAC | 1027 |
| Thr | Gly | Gly | Lys | Gln | Arg | Ser | Gln | Asn | Arg | Ser | Lys | Thr | Pro | Lys | Asn |      |
|     |     | 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |     |     |      |

08937756 092597

CAA GAG GCC CTG AGG ATG GCC AGT GTG GCA GAA AAC AGC AGC AGT GAC 1075  
 Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser Asp  
 310 315 320

CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC 1123  
 Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp  
 325 330 335 340

CTT GGC TGG CAG GAC TGG ATC ATT GCA CCT GAA GGC TAT GCT GCC TAC 1171  
 Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr  
 345 350 355

TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC 1219  
 Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala  
 360 365 370

ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC 1267  
 Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp  
 375 380 385

ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT 1315  
 Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser  
 390 395 400

GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA 1363  
 Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg  
 405 410 415 420

AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCTG 1413  
 Asn Met Val Val Arg Ala Cys Gly Cys His  
 425 430

ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG 1473

CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACC TCCCAACCGG 1533

AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT 1593

GGCACGTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT 1653

GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCTTGGC GCTCTGAGTC TTTGAGGAGT 1713

AATCGCAAGC CTCGTTTACG TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GCGCTGGCG 1773

TCTGTGTTGA AGGGAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT 1833

GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC 1873

009375-092597



(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /product= "mOP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1             5             10             15

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
      20             25             30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
      35             40             45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
      50             55             60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
      65             70             75             80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly
      85             90             95

Pro Asp Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr
      100            105            110

Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp
      115            120            125

Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu
      130            135            140

Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser
      145            150            155            160

Lys Ile Pro Glu Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr
      165            170            175

Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr
      180            185            190

Val Tyr Gln Val Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe
      195            200            205

```

0993756-09937

Leu Leu Asp Ser Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val  
 210 215 220  
 Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His  
 225 230 235 240  
 Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile  
 245 250 255  
 Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys  
 260 265 270  
 Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg  
 275 280 285  
 Ser Ile Arg Ser Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys  
 290 295 300  
 Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn  
 305 310 315 320  
 Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val  
 325 330 335  
 Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly  
 340 345 350  
 Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser  
 355 360 365  
 Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe  
 370 375 380  
 Ile Asn Pro Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu  
 385 390 395 400  
 Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu  
 405 410 415  
 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His  
 420 425 430

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

265260" 9542680

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens  
(F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 490..1696  
(D) OTHER INFORMATION: /note= "hOP2 (cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

GGCGCCGGCA GAGCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGAGG TGGCACGGCA      60
GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCAGG AGGCGCTGGA GCAACAGCTC      120
CCACACCGCA CCAAGCGGTG GCTGCAGGAG CTCGCCATC GCCCTGCGC TGCTCGGACC      180
GCGGCCACAG CCGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCCGA GAGTCCCAGT      240
CCGCAGAGTA GCGCCGGCCT CGAGGCGGTG GCGTCCCGGT CCTCTCCGTC CAGGAGCCAG      300
GACAGGTGTC GCGCGGCGGG GCTCCAGGGA CCGCGCCTGA GGCCGGCTGC CCGCCCGTCC      360
CGCCCCGCCC CGCCGCCCCG CGCCGCGCGA GCCCAGCCTC CTGCGCGTCG GGGCGTCCCC      420
AGGCCCTGGG TCGGCGCGG AGCCGATGCG CGCCGCTGA GCGCCCCAGC TGAGCGCCCC      480
CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG      528
      Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu
          1             5             10

GCG CTA TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA CCC CCG CCC      576
Ala Leu Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro
      15             20             25

GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG      624
Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln
      30             35             40             45

CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC      672
Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg
          50             55             60

GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG      720
Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met
          65             70             75

CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG      768
Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala
      80             85             90

```

0893756.092597

|   |      |
|---|------|
| CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT<br>Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val<br>95 100 105      | 816  |
| AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG<br>Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp<br>110 115 120 125 | 864  |
| AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC<br>Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val<br>130 135 140     | 912  |
| ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC<br>Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu<br>145 150 155     | 960  |
| AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC<br>Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser<br>160 165 170     | 1008 |
| AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT<br>Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala<br>175 180 185     | 1056 |
| GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC<br>Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys<br>190 195 200 205 | 1104 |
| TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG<br>Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu<br>210 215 220     | 1152 |
| ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT<br>Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly<br>225 230 235     | 1200 |
| CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG<br>Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg<br>240 245 250     | 1248 |
| GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG<br>Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg<br>255 260 265     | 1296 |
| AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC AAC CGA CTC<br>Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu<br>270 275 280 285 | 1344 |
| CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG GTC TGC<br>Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys<br>290 295 300     | 1392 |

00937756-002597

CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC 1440  
Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp  
305 310 315

TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG 1488  
Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu  
320 325 330

TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC ATC 1536  
Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile  
335 340 345

CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG 1584  
Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala  
350 355 360 365

TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC 1632  
Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp  
370 375 380

AGC AGC AAC AAC GTC ATC CTG CGC AAA CAC CGC AAC ATG GTG GTC AAG 1680  
Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys  
385 390 395

GCC TGC GGC TGC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG 1723  
Ala Cys Gly Cys His  
400

(2) INFORMATION FOR SEQ ID NO:21:

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

(A)OTHER INFORMATION: /product= "hOP2-PP"

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys  
1 5 10 15

Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro  
20 25 30

Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile  
35 40 45

0893756.09259

Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro  
 50 55 60  
 Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu  
 65 70 75 80  
 Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu  
 85 90 95  
 Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val  
 100 105 110  
 Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe  
 115 120 125  
 Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala  
 130 135 140  
 Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr  
 145 150 155 160  
 Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu  
 165 170 175  
 Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu  
 180 185 190  
 Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu  
 195 200 205  
 Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp  
 210 215 220  
 Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala  
 225 230 235 240  
 Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro  
 245 250 255  
 Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Gln  
 260 265 270  
 Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile  
 275 280 285  
 Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His  
 290 295 300  
 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile  
 305 310 315 320

465260-9544680

Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe  
325 330 335

Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser  
340 345 350

Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala  
355 360 365

Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn  
370 375 380

Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly  
385 390 395 400

Cys His

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1926 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: MURIDAE  
(F) TISSUE TYPE: EMBRYO

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 93..1289  
(D) OTHER INFORMATION: /note= "mOP2 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|   |     |
|---|-----|
| GCCAGGCACA GGTGCGCCGT CTGGTCCTCC CCGTCTGGCG TCAGCCGAGC          | 50  |
| CCGACCAGCT ACCAGTGGAT GCGCGCCGGC TGAAAGTCCG AG ATG GCT ATG CGT  | 104 |
| Met Ala Met Arg   |     |
| 1   |     |
| CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG TGC GCG CTG GGA GGC | 152 |
| Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly |     |
| 5 10 15 20  |     |
| GGC CAC GGT CCG CGT CCC CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA | 200 |
| Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly |     |
| 25 30 35  |     |

08937756.092597

|  |     |
|--|-----|
| CGC CGC GAG CGC CGC GAC ATG CAG CGT GAA ATC CTG GCG GTG CTC GGG<br>Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly | 248 |
| 40<br>50   |     |
| CTA CCG GGA CGG CCC CGA CCC CGT GCA CAA CCC GCG GCT GCC CGG CAG<br>Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Arg Gln     | 296 |
| 55<br>65   |     |
| CCA GCG TCC GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC<br>Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr | 344 |
| 70<br>80   |     |
| GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC<br>Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp | 392 |
| 85<br>90<br>100  |     |
| CTG GTC ATG AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC<br>Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly | 440 |
| 105<br>110<br>115  |     |
| TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC<br>Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile | 488 |
| 120<br>125<br>130  |     |
| CCT GCT GGG GAG GCT GTC ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA<br>Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu | 536 |
| 135<br>140<br>145  |     |
| CCC AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA<br>Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu | 584 |
| 150<br>155<br>160  |     |
| GTG GTC CAA GAG CAC TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT<br>Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp | 632 |
| 165<br>170<br>175<br>180   |     |
| CTT CAG ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG CTG GAC ATC<br>Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu Asp Ile | 680 |
| 185<br>190<br>195  |     |
| ACA GCA GCC AGT GAC CGA TGG CTG CTG AAC CAT CAC AAG GAC CTG GGA<br>Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly | 728 |
| 200<br>205<br>210  |     |
| CTC CGC CTC TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT CCT GGC<br>Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly | 776 |
| 215<br>220<br>225  |     |
| CTG GCT GGT CTG CTT GGA CGA CAA GCA CCA CGC TCC AGA CAG CCT TTC<br>Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe | 824 |
| 230<br>235<br>240  |     |



|   |      |
|---|------|
| ATG GTA ACC TTC TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT CGG<br>Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg<br>245 250 255 260 | 872  |
| GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA AAG AAA ACG AAC GAG CTT<br>Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu<br>265 270 275     | 920  |
| CCG CAC CCC AAC AAA CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC<br>Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser<br>280 285 290     | 968  |
| CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC TAC GTC AGC TTC CGT<br>Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg<br>295 300 305     | 1016 |
| GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC<br>Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala<br>310 315 320     | 1064 |
| TAT TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC TCC TGT ATG AAC<br>Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn<br>325 330 335 340 | 1112 |
| GCC ACC AAC CAT GCC ATC TTG CAG TCT CTG GTG CAC CTG ATG AAG CCA<br>Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro<br>345 350 355     | 1160 |
| GAT GTT GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG AGT GCC ACC<br>Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr<br>360 365 370     | 1208 |
| TCT GTG CTG TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CGT AAA CAC<br>Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His<br>375 380 385     | 1256 |
| CGT AAC ATG GTG GTC AAG GCC TGT GGC TGC CAC TGAGGCCCCG CCCAGCATCC<br>Arg Asn Met Val Val Lys Ala Cys Gly Cys His<br>390 395                           | 1309 |
| TGCTTCTACT ACCTTACCAT CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT   | 1369 |
| TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTCCTGTCTA   | 1429 |
| AAATTCTGGT CTTTCCCAGT TCCTCTGTCC TTCATGGGGT TTCGGGGGCTA TCACCCCGCC  | 1489 |
| CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA   | 1549 |
| ACTGAGAGGT CTGGGGTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC   | 1609 |
| CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGGC CGTGGAATTC TAACTAGAT  | 1669 |

0097-686 : 090609

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 399 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(D) OTHER INFORMATION: /product= "mOP2-PP"

Met Ala Met Arg Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys  
1 5 10 15

Ala Leu Gly Gly Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln  
20 25 30

Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala  
35 40 45

Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala  
50 55 60 65

Ala Arg Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala  
70 75 80

Met Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg  
85 90 95

Ala Asp Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr  
100 105 110

Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr  
115 120 125 130

Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr  
135 140 145

Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met  
150 155 160

Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe  
165 170 175

Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu  
180 185 190

Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp  
195 200 205 210

Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp  
215 220 225

Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln  
230 235 240

Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala  
245 250 255

Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn  
260 265 270

Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His  
275 280 285 290

Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser  
295 300 305

Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr  
310 315 320

Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys  
325 330 335

Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met  
340 345 350

Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser  
355 360 365 370

Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg  
375 380 385

Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His  
390 395

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1368 base pairs

00937756.092597

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1368
- (D) OTHER INFORMATION: /STANDARD NAME="60A"

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: WHARTON, KRISTI A.; THOMSEN, GERALD H.; GELBERT, WILLIAM M.
- (B) TITLE: DROSOPHILA 60A GENE...
- (C) JOURNAL: PROC. NAT'L ACAD. SCI. USA
- (D) VOLUME: 88
- (E) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1368
- (F) PAGES: 9214-9218
- (G) DATE: OCT - 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|   |     |
|---|-----|
| ATG TCG GGA CTG CGA AAC ACC TCG GAG GCC GTT GCA GTG CTC GCC TCC | 48  |
| Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser |     |
| 1 5 10 15   |     |
| CTG GGA CTC GGA ATG GTT CTG CTC ATG TTC GTG GCG ACC ACG CCG CCG | 96  |
| Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro |     |
| 20 25 30  |     |
| GCC GTT GAG GCC ACC CAG TCG GGG ATT TAC ATA GAC AAC GGC AAG GAC | 144 |
| Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp |     |
| 35 40 45  |     |
| CAG ACG ATC ATG CAC AGA GTG CTG AGC GAG GAC GAC AAG CTG GAC GTC | 192 |
| Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val |     |
| 50 55 60  |     |
| TCG TAC GAG ATC CTC GAG TTC CTG GGC ATC GCC GAA CGG CCG ACG CAC | 240 |
| Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His |     |
| 65 70 75 80   |     |
| CTG AGC AGC CAC CAG TTG TCG CTG AGG AAG TCG GCT CCC AAG TTC CTG | 288 |
| Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu |     |
| 85 90 95  |     |
| CTG GAC GTC TAC CAC CGC ATC ACG GCG GAG GAG GGT CTC AGC GAT CAG | 336 |
| Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln |     |
| 100 105 110   |     |

08937756-092597

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| GAT<br>Asp        | GAG<br>Glu        | GAC<br>Asp<br>115 | GAC<br>Asp        | GAC<br>Asp        | TAC<br>Tyr        | GAA<br>Glu        | CGC<br>Arg<br>120 | GGC<br>Gly        | CAT<br>His        | CGG<br>Arg        | TCC<br>Ser        | AGG<br>Arg<br>125 | AGG<br>Arg        | AGC<br>Ser        | GCC<br>Ala        | 384 |
| GAC<br>Asp        | CTC<br>Leu<br>130 | GAG<br>Glu        | GAG<br>Glu        | GAT<br>Asp        | GAG<br>Glu        | GGC<br>Gly<br>135 | GAG<br>Glu        | CAG<br>Gln        | CAG<br>Gln        | AAG<br>Lys        | AAC<br>Asn<br>140 | TTC<br>Phe        | ATC<br>Ile        | ACC<br>Thr        | GAC<br>Asp        | 432 |
| CTG<br>Leu<br>145 | GAC<br>Asp        | AAG<br>Lys        | CGG<br>Arg        | GCC<br>Ala        | ATC<br>Ile<br>150 | GAC<br>Asp        | GAG<br>Glu        | AGC<br>Ser        | GAC<br>Asp        | ATC<br>Ile<br>155 | ATC<br>Ile        | ATG<br>Met        | ACC<br>Thr        | TTC<br>Phe        | CTG<br>Leu<br>160 | 480 |
| AAC<br>Asn        | AAG<br>Lys        | CGC<br>Arg        | CAC<br>His        | CAC<br>His<br>165 | AAT<br>Asn        | GTG<br>Val        | GAC<br>Asp        | GAA<br>Glu        | CTG<br>Leu<br>170 | CGT<br>Arg        | CAC<br>His        | GAG<br>Glu        | CAC<br>His        | GGC<br>Gly<br>175 | CGT<br>Arg        | 528 |
| CGC<br>Arg        | CTG<br>Leu        | TGG<br>Trp        | TTC<br>Phe<br>180 | GAC<br>Asp        | GTC<br>Val        | TCC<br>Ser        | AAC<br>Asn        | GTG<br>Val<br>185 | CCC<br>Pro        | AAC<br>Asn        | GAC<br>Asp        | AAC<br>Asn        | TAC<br>Tyr<br>190 | CTG<br>Leu        | GTG<br>Val        | 576 |
| ATG<br>Met        | GCC<br>Ala        | GAG<br>Glu<br>195 | CTG<br>Leu        | CGC<br>Arg        | ATC<br>Ile        | TAT<br>Tyr        | CAG<br>Gln<br>200 | AAC<br>Asn        | GCC<br>Ala        | AAC<br>Asn        | GAG<br>Glu        | GGC<br>Gly<br>205 | AAG<br>Lys        | TGG<br>Trp        | CTG<br>Leu        | 624 |
| ACC<br>Thr        | GCC<br>Ala<br>210 | AAC<br>Asn        | AGG<br>Arg        | GAG<br>Glu        | TTC<br>Phe<br>215 | ACC<br>Thr        | ATC<br>Ile        | ACG<br>Thr        | GTA<br>Val        | TAC<br>Tyr        | GCC<br>Ala<br>220 | ATT<br>Ile        | GGC<br>Gly        | ACC<br>Thr        | GGC<br>Gly        | 672 |
| ACG<br>Thr<br>225 | CTG<br>Leu        | GGC<br>Gly        | CAG<br>Gln        | CAC<br>His        | ACC<br>Thr<br>230 | ATG<br>Met        | GAG<br>Glu        | CCG<br>Pro        | CTG<br>Leu        | TCC<br>Ser<br>235 | TCG<br>Ser        | GTG<br>Val        | AAC<br>Asn        | ACC<br>Thr        | ACC<br>Thr<br>240 | 720 |
| GGG<br>Gly        | GAC<br>Asp        | TAC<br>Tyr        | GTG<br>Val        | GGC<br>Gly<br>245 | TGG<br>Trp        | TTG<br>Leu        | GAG<br>Glu        | CTC<br>Leu        | AAC<br>Asn<br>250 | GTG<br>Val        | ACC<br>Thr        | GAG<br>Glu        | GGC<br>Gly        | CTG<br>Leu<br>255 | CAC<br>His        | 768 |
| GAG<br>Glu        | TGG<br>Trp        | CTG<br>Leu        | GTC<br>Val<br>260 | AAG<br>Lys        | TCG<br>Ser        | AAG<br>Lys        | GAC<br>Asp        | AAT<br>Asn<br>265 | CAT<br>His        | GGC<br>Gly        | ATC<br>Ile        | TAC<br>Tyr        | ATT<br>Ile<br>270 | GGA<br>Gly        | GCA<br>Ala        | 816 |
| CAC<br>His        | GCT<br>Ala        | GTC<br>Val<br>275 | AAC<br>Asn        | CGA<br>Arg        | CCC<br>Pro        | GAC<br>Asp        | CGC<br>Arg<br>280 | GAG<br>Glu        | GTG<br>Val        | AAG<br>Lys        | CTG<br>Leu<br>285 | GAC<br>Asp        | GAC<br>Asp        | ATT<br>Ile        | GGA<br>Gly        | 864 |
| CTG<br>Leu        | ATC<br>Ile<br>290 | CAC<br>His        | CGC<br>Arg        | AAG<br>Lys        | GTG<br>Val<br>295 | GAC<br>Asp        | GAC<br>Asp        | GAG<br>Glu        | TTC<br>Phe        | CAG<br>Gln<br>300 | CCC<br>Pro        | TTC<br>Phe        | ATG<br>Met        | ATC<br>Ile        | GGC<br>Gly        | 912 |
| TTC<br>Phe<br>305 | TTC<br>Phe        | CGC<br>Arg        | GGA<br>Gly        | CCG<br>Pro        | GAG<br>Glu<br>310 | CTG<br>Leu        | ATC<br>Ile        | AAG<br>Lys        | GCG<br>Ala        | ACG<br>Thr<br>315 | GCC<br>Ala        | CAC<br>His        | AGC<br>Ser        | AGC<br>Ser        | CAC<br>His<br>320 | 960 |

|   |      |
|---|------|
| CAC AGG AGC AAG CGA AGC GCC AGC CAT CCA CGC AAG CGC AAG AAG TCG | 1008 |
| His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser |      |
| 325 330 335   |      |
| GTG TCG CCC AAC AAC GTG CCG CTG CTG GAA CCG ATG GAG AGC ACG CGC | 1056 |
| Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg |      |
| 340 345 350   |      |
| AGC TGC CAG ATG CAG ACC CTG TAC ATA GAC TTC AAG GAT CTG GGC TGG | 1104 |
| Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp |      |
| 355 360 365   |      |
| CAT GAC TGG ATC ATC GCA CCA GAG GGC TAT GGC GCC TTC TAC TGC AGC | 1152 |
| His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser |      |
| 370 375 380   |      |
| GGC GAG TGC AAT TTC CCG CTC AAT GCG CAC ATG AAC GCC ACG AAC CAT | 1200 |
| Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His |      |
| 385 390 395 400   |      |
| GCG ATC GTC CAG ACC CTG GTC CAC CTG CTG GAG CCC AAG AAG GTG CCC | 1248 |
| Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro |      |
| 405 410 415   |      |
| AAG CCC TGC TGC GCT CCG ACC AGG CTG GGA GCA CTA CCC GTT CTG TAC | 1296 |
| Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr |      |
| 420 425 430   |      |
| CAC CTG AAC GAC GAG AAT GTG AAC CTG AAA AAG TAT AGA AAC ATG ATT | 1344 |
| His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile |      |
| 435 440 445   |      |
| GTG AAA TCC TGC GGG TGC CAT TGA                                 | 1368 |
| Val Lys Ser Cys Gly Cys His                                     |      |
| 450 455   |      |

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 455 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Leu | Arg | Asn | Thr | Ser | Glu | Ala | Val | Ala | Val | Leu | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

10937756-09397

Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro  
 20 25 30  
 Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp  
 35 40 45  
 Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val  
 50 55 60  
 Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His  
 65 70 75 80  
 Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu  
 85 90 95  
 Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln  
 100 105 110  
 Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala  
 115 120 125  
 Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp  
 130 135 140  
 Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu  
 145 150 155 160  
 Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg  
 165 170 175  
 Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val  
 180 185 190  
 Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu  
 195 200 205  
 Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly  
 210 215 220  
 Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr  
 225 230 235 240  
 Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His  
 245 250 255  
 Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala  
 260 265 270  
 His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly  
 275 280 285  
 Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly  
 290 295 300

00937756.09369

Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His  
 305 310 315 320  
 His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser  
 325 330 335  
 Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg  
 340 345 350  
 Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp  
 355 360 365  
 His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser  
 370 375 380  
 Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His  
 385 390 395 400  
 Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro  
 405 410 415  
 Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr  
 420 425 430  
 His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile  
 435 440 445  
 Val Lys Ser Cys Gly Cys His  
 450 455

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note="BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid

165260" 9572680





**(ix) FEATURE:**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Thr Val Glu Ser Cys Ala Cys Arg  
100

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vii) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

(ix) **FEATURE:**

(A) NAME/KEY: Protein  
(B) LOCATION: 1..102  
(D) OTHER INFORMATION: /note= "BMP5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln  
 1 5 10 15  
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly  
 20 25 30  
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala  
 35 40 45  
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys  
 50 55 60  
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe  
 65 70 75 80  
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val  
 85 90 95  
 Arg Ser Cys Gly Cys His  
 100

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..102  
 (D) OTHER INFORMATION: /note= "BMP6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln  
 1 5 10 15  
 Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly  
 20 25 30  
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala  
 35 40 45

265260-9572680

Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys  
 50 55 60  
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe  
 65 70 75 80  
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Trp Met Val Val  
 85 90 95  
 Arg Ala Cys Gly Cys His  
 100

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= OPX  
 /note= "WHEREIN XAA AT EACH POS'N IS INDEPENDENTLY  
 SELECTED FROM THE RESIDUES OCCURRING AT THE  
 CORRESPONDING POS'N IN THE C-TERMINAL SEQUENCE OF MOUSE  
 OR HUMAN OP1 OR OP2 (SEE SEQ. ID NOS. 5,6,7 and 8 or  
 16,18,20 and 22.)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa  
 1 5 10 15  
 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly  
 20 25 30  
 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala  
 35 40 45  
 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys  
 50 55 60

265260" 952680

Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa  
65 70 75 80  
Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val  
85 90 95  
Xaa Ala Cys Gly Cys His  
100

(2) INFORMATION FOR SEQ ID NO:30:

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

- (A) NAME: Generic Sequence 5
- (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:30:

Leu Xaa Xaa Xaa Phe  
1 5  
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa  
10  
Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala  
15 20  
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa  
25 30  
Xaa Pro Xaa Xaa Xaa Xaa Xaa  
35  
Xaa Xaa Xaa Asn His Ala Xaa Xaa  
40 45  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
55 60  
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa  
65  
Xaa Xaa Xaa Leu Xaa Xaa Xaa  
70 75  
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa  
80  
Xaa Xaa Xaa Xaa Met Xaa Val Xaa  
85 90  
Xaa Cys Xaa Cys Xaa  
95

265260-952680

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 6

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe

**1                      5                      10**

Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

15

Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala

20 25

Xaa Tyr Cys Xaa Gly Xaa Cys Xaa

30 35

Xaa Pro Xaa Xaa Xaa Xaa Xaa

40

Xaa Xaa Xaa Asn His Ala Xaa Xaa

45 50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

55

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

60 65

Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

70

Xaa Xaa Xaa Leu Xaa Xaa Xaa

75 80

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

85

Xaa Xaa Xaa Xaa Met Xaa Val Xaa

90

95

Xaa Cys Xaa Cys Xaa

100

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1238 base pairs, 372 amino acids
- (B) TYPE: nucleic acid, amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (F) TISSUE TYPE: BRAIN

(iv) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:

(D) OTHER INFORMATION:

/product= "GDF-1"  
/note= "GDF-1 CDNA"

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Lee, Se-Jin
- (B) TITTLE: Expression of Growth/Differentiation Factor 1
- (C) JOURNAL: Proc. Nat'l Acad. Sci.
- (D) VOLUME: 88
- (E) RELEVANT RESIDUES: 1-1238
- (F) PAGES: 4250-4254
- (G) DATE: May-1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGGACACCG GCCCGGCCCT CAGCCCACTG GTCCCGGGCC GCCGCGGACC CTGCGCACTC 60

TCTGGTCATC GCCTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC GGC 113  
Met Pro Pro Pro Gln Gln Gly Pro Cys Gly  
1 5 10

CAC CAC CTC CTC CTC CTC CTG GCC CTG CTG CTG CCC TCG CTG CCC 158  
His His Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro  
15 20 25

465260"957680

|  |     |
|--|-----|
| CTG ACC CGC GCC CCC GTG CCC CCA GGC CCA GCC GCC GCC CTG CTC<br>Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu | 203 |
| 30 35 40   |     |
| CAG GCT CTA GGA CTG CGC GAT GAG CCC CAG GGT GCC CCC AGG CTC<br>Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu | 248 |
| 45 50 55   |     |
| CGG CCG GTT CCC CCG GTC ATG TGG CGC CTG TTT CGA CGC CGG GAC<br>Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp | 293 |
| 60 65 70   |     |
| CCC CAG GAG ACC AGG TCT GGC TCG CGG CGG ACG TCC CCA GGG GTC<br>Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val | 338 |
| 75 80 85   |     |
| ACC CTG CAA CCG TGC CAC GTG GAG GAG CTG GGG GTC GCC GGA AAC<br>Thr Leu Gln Pro Cys His Val Glu Glu Leu Gly Val Ala Gly Asn | 383 |
| 90 95 100  |     |
| ATC GTG CGC CAC ATC CCG GAC CGC GGT GCG CCC ACC CGG GCC TCG<br>Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser | 428 |
| 105 110 115  |     |
| GAG CCT GTC TCG GCC GCG GGG CAT TGC CCT GAG TGG ACA GTC GTC<br>Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr Val Val | 473 |
| 120 125 130  |     |
| TTC GAC CTG TCG GCT GTG GAA CCC GCT GAG CGC CCG AGC CGG GCC<br>Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg Ala | 518 |
| 135 140 145  |     |
| CGC CTG GAG CTG CGT TTC GCG GCG GCG GCG GCG GCA GCC CCG GAG<br>Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Ala Pro Glu | 563 |
| 150 155 160  |     |
| GGC GGC TGG GAG CTG AGC GTG GCG CAA GCG GGC CAG GGC GCG GGC<br>Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly | 608 |
| 165 170 175  |     |
| GCG GAC CCC GGG CCG GTG CTG CTC CGC CAG TTG GTG CCC GCC CTG<br>Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu | 653 |
| 180 185 190  |     |
| GGG CCG CCA GTG CGC GCG GAG CTG CTG GGC GCC GCT TGG GCT CGC<br>Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg | 698 |
| 195 200 205  |     |
| AAC GCC TCA TGG CCG CGC AGC CTC CGC CTG GCG CTG GCG CTA CGC<br>Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg | 743 |
| 210 215 220  |     |

00937756-09397

|  |      |
|--|------|
| CCC CGG GCC CCT GCC GCC TGC GCG CGC CTG GCC GAG GCC TCG CTG  | 788  |
| Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu  |      |
| 225 230 235  |      |
| CTG CTG GTG ACC CTC GAC CCG CGC CTG TGC CAC CCC CTG GCC CGG  | 833  |
| Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg  |      |
| 240 245 250  |      |
| CCG CGG CGC GAC GCC GAA CCC GTG TTG GGC GGC GGC CCC GGG GGC  | 878  |
| Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly  |      |
| 255 260 265  |      |
| GCT TGT CGC GCG CGG CGG CTG TAC GTG AGC TTC CGC CAG GTG GGC  | 923  |
| Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly  |      |
| 270 275 280  |      |
| TGG CAC CGC TGG GTC ATC GCG CCG CGC CCC TTC CTG GCC AAC TAC  | 968  |
| Trp His Arg Trp Val Ile Arg Pro Arg Gly Phe Leu Ala Asn Tyr  |      |
| 285 290 295  |      |
| TGC CAG GGT CAG TGC GCG CTG CCC GTC GCG CTG TCG GGG TCC GGG  | 1013 |
| Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly  |      |
| 300 305 310  |      |
| GGG CCG CCG GCG CTC AAC CAC GCT GTG CTG CGC GCG CTC ATG CAC  | 1058 |
| Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His  |      |
| 315 320 325  |      |
| GCG GCC GCC CCG GGA GCC GCC GAC CTG CCC TGC TGC GTG CCC GCG  | 1103 |
| Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala  |      |
| 330 335 340  |      |
| CGC CTG TCG CCC ATC TCC GTG CTC TTC TTT GAC AAC AGC GAC AAC  | 1148 |
| Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn  |      |
| 345 350 355  |      |
| GTG GTG CTG CGG CAG TAT GAG GAC ATG GTG GTG GAC GAG TGC GGC  | 1193 |
| Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly  |      |
| 360 365 370  |      |
| TGC CGC TAACCCGGGG CGGGCAGGGA CCCGGGCCCA ACAATAAATG CCGCGTGG | 1238 |
| Cys Arg  |      |
| 372  |      |

(34) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

08937756-092597



- (ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(v) ORIGINAL SOURCE:  
    (A) ORGANISM: human  
    (F) TISSUE TYPE: BRAIN  
(ix) FEATURE:  
    (A) NAME/KEY: CDS  
    (B) LOCATION:  
    (D) OTHER INFORMATION: /function=  
                              /product= "GDF-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | Met | Pro | Pro | Pro | Gln | Gln | Gly | Pro | Cys | Gly |     |
|     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |
| His | His | Leu | Leu | Leu | Leu | Leu | Ala | Leu | Leu | Pro | Ser |
|     |     |     |     | 15  |     |     |     | 20  |     |     | 25  |
| Leu | Thr | Arg | Ala | Pro | Val | Pro | Pro | Gly | Pro | Ala | Ala |
|     |     |     |     | 30  |     |     |     | 35  |     |     | 40  |
| Gln | Ala | Leu | Gly | Leu | Arg | Asp | Glu | Pro | Gln | Gly | Ala |
|     |     |     |     | 45  |     |     |     | 50  |     |     | 55  |
| Arg | Pro | Val | Pro | Pro | Val | Met | Trp | Arg | Leu | Phe | Arg |
|     |     |     |     | 60  |     |     |     | 65  |     |     | 70  |
| Pro | Gln | Glu | Thr | Arg | Ser | Gly | Ser | Arg | Arg | Thr | Ser |
|     |     |     |     | 75  |     |     |     | 80  |     |     | 85  |
| Thr | Leu | Gln | Pro | Cyc | His | Val | Glu | Glu | Leu | Gly | Val |
|     |     |     |     | 90  |     |     |     |     | 95  |     | 100 |
| Ile | Val | Arg | His | Ile | Pro | Asp | Arg | Gly | Ala | Pro | Thr |
|     |     |     |     | 105 |     |     |     |     | 110 |     | 115 |
| Glu | Pro | Val | Ser | Ala | Ala | Gly | His | Cys | Pro | Glu | Trp |
|     |     |     |     | 120 |     |     |     |     | 125 |     | 130 |
| Phe | Asp | Leu | Ser | Ala | Val | Glu | Pro | Ala | Glu | Arg | Pro |
|     |     |     |     | 135 |     |     |     |     | 140 |     | 145 |
| Arg | Leu | Glu | Leu | Arg | Phe | Ala | Ala | Ala | Ala | Ala | Pro |
|     |     |     |     | 150 |     |     |     |     | 155 |     | 160 |

00937756-002597

Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly  
165 170 175

Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu  
180 185 190

Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg  
195 200 205

Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg  
210 215 220

Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu  
225 230 235

Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg  
240 245 250

Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly  
255 260 265

Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly  
270 275 280

Trp His Arg Trp Val Ile Arg Pro Arg Gly Phe Leu Ala Asn Tyr  
285 290 295

Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly  
300 305 310

Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His  
315 320 325

Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala  
330 335 340

Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn  
345 350 355

Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly  
360 365 370

Cys Arg  
372

08937756-089597